AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions and listing of claims in the application.

1. **(currently amended)** A method for finding translation initiation codons in a nucleotide sequence, comprising:

a) analyzing a first data set to measure a combination of features of initiator codons and pseudoinitiator codons [[and]] to produce ~~a set of numerical values~~ **scoring function parameters** for said combination of features; [[and]]

b) ~~evaluating scoring functions by~~ reading a sequence in the vicinity of an ATG triplet and using [[said]] **one or more** scoring functions and [[said]] **one or more of the** scoring ~~function's~~ **function** parameters to ~~return~~ **determine** a numerical score that quantifies how much said ATG triplet resembles an initiator codon; [[and]]

c) **using Quadratic Discriminant Analysis** ~~generating a quadratic discriminant function through selection of~~ **with** a combination of feature variables that optimally ~~classifies~~ **classify** ATG triplets in a nucleotide sequence as initiator codons or as pseudoinitiator codons based on the ~~output of said scoring functions~~ **numerical score determined in step b) to generate a quadratic discriminant function** ~~and through the use of Quadratic Discriminant Analysis~~; and

d) **analyzing a second data set of nucleotide sequences** using said quadratic discriminant function ~~to analyze a second data set of nucleotide sequences by evaluating~~**, wherein said analysis comprises evaluating** at least one scoring function for each ATG triplet in said sequences [[and]] to calculate the probability **whether each**

ATG triplet is [[of]] an initiator codon ~~at a position using the output of said analysis~~; and

e) locating translation initiation codons in said second data set based on the probability calculated in step d).

2. (original) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of features from step a) comprises at least two of the features provided in Table 1.

3. (original) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said scoring functions from step d) comprise at least two of the scoring functions provided in Table 2.

4. (currently amended) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of feature variables from step c) comprises any combination of at least two of the feature variables provided in Table 3 wherein the combination comprises one feature variable from each of any two feature variable classes and results in a correlation coefficient for the feature variable combination [[of]] greater than 0.9.

5. (currently amended) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of feature variables from step c) comprises any combination of at least two of the feature variables provided

in Table 3 wherein the combination comprises one feature variable from each of any two

feature variable classes and results in a correlation coefficient for the feature variable

combination [[of]] greater than 0.8.